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School of Computer Science & Engineering

IILM University Greater Noida

Presents

1st National Conference

on

Technologies for Sustainable Development Goals 2025 (TECH4SDG-2025)

3rd March 2025

Technically Co-Sponsored by IEEE UP SECTION (INDIA)

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INTERNATIONAL JOURNAL OF RESEARCH IN MODERN ENGINEERING & EMERGING TECHNOLOGY (IJRMEET)

Dear Author / Researcher,

On behalf of the *International Journal of Research in Modern Engineering & Emerging Technology (IJRMEET)*, I extend my heartfelt gratitude to all the authors and research scholars for choosing our platform to publish their valuable research contributions.

IJRMEET, a Refereed, Peer Reviewed, Indexed, and Monthly Journal in Electronic format, has been consistently dedicated since April 2013 to advancing scholarly work in the domains of Modern Engineering and Emerging Technologies. Your innovative and quality research is at the core of our mission to promote academic excellence and practical solutions in the ever-evolving field of engineering and technology.

We believe that publication should be based purely on the merit, originality, and relevance of the research, not on financial considerations. We ensure that every manuscript undergoes a thorough review process to maintain the integrity, reliability, and scholarly value of each published work.

Our journal aims not only to disseminate high-quality research globally but also to highlight critical engineering problems and their practical resolutions. I encourage researchers, academicians, faculty members, and industry professionals to continue contributing to IJRMEET and to inspire their peers and students to join us in this academic pursuit.

We sincerely thank our respected Editors, Reviewers, Technical Advisors, Authors, Web Developers, Subscribers, Supporters, and the extended academic community whose efforts and encouragement make each issue of IJRMEET a successful endeavor.

With warm regards,

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डॉ. मोहम्मद रिहान / Dr. Mohammad Rihan
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MESSAGE

I am happy to know about Tech4SDG-2025, a distinguished national conference that aims to explore and highlight the transformative power of technology in achieving the United Nations Sustainable Development Goals (SDGs). This event serves as a critical platform for fostering collaboration among experts, innovators, and leaders who are dedicated to creating solutions that drive sustainable change.

As we face global challenges ranging from environmental sustainability to social equity, it is clear that technological advancements will play a pivotal role in shaping our collective future. Tech4SDG-2025 presents a unique opportunity to examine how cutting-edge technologies can contribute to solving the most pressing issues of our time, from climate change to poverty alleviation.

I look forward to the engaging discussions and innovative ideas that will emerge from this conference. I believe that by working together, we can harness the potential of technology to drive meaningful progress towards a sustainable and equitable world.

I extend my best wishes to all the participants and organizers of Tech4SDG-2025.

27.02.25

(Dr. Mohammad Rihan)

Dated: 27th February, 2025
Place: Gurugram

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Influence of Household Water Sources on Basic Microbial Diversity

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Abstract : Households obtain drinking water from piped supply, boreholes, hand pumps, open wells and storage containers, and each source carries its own microbial community. This study examined how the source of household water influences basic microbial diversity and contamination. A total of 120 water samples, 24 from each of five source types, were analysed for total plate count, total coliforms, Escherichia coli, turbidity and bacterial genera present, and the Shannon diversity index of genera was calculated. Total plate count rose from 2.3 log CFU/mL in piped water to 4.3 in open wells ($F(4, 115) = 30.9$, $p < 0.001$). Shannon diversity followed the same order, from 1.12 to 1.88 ($F(4, 115) = 32.2$, $p < 0.001$). E. coli was found in 8.3% of piped samples, 16.7% of borewell samples, 29.2% of hand-pump samples, 62.5% of open-well samples and 45.8% of stored samples ($\chi^2 = 21.0$, $p < 0.001$). Turbidity was strongly related to bacterial load across sources. Pseudomonas and Bacillus were found in all sources, while faecal indicator and opportunistic genera were concentrated in open wells and stored water. Water source is a major determinant of the microbial quality and diversity of household water, and protection of sources and safe storage should be prioritised.

Keywords: household water; microbial diversity; total coliforms; Escherichia coli; Shannon index; water quality; point-of-use

Introduction

Safe drinking water is a basic requirement for health, and microbial contamination remains the main threat to its safety. Contaminated water causes diarrhoeal disease and other infections, and the burden falls most heavily on children in places where sanitation is poor (Bartram & Cairncross, 2010). Systematic reviews have found that a substantial share of the global population uses drinking water that is contaminated with faecal bacteria, with the problem greatest in low-income settings and among unprotected sources (Bain et al., 2014).

In India and many other countries, households draw water from several types of source. Municipal supply reaches some, while others depend on borewells, hand pumps, open dug wells, ponds or tankers. Water is then commonly stored in vessels at home. Each source differs in its exposure to contamination, its depth and the treatment it receives, and therefore in the microbial community that it carries. Water is never sterile: even treated drinking water contains a natural community of harmless bacteria, and the question of public health importance is how the size and composition of this community, and the presence of pathogens and indicators, vary between sources.

Microbial diversity gives an additional view. The diversity of a community, measured by how many kinds of organism are present and how evenly they are distributed, can indicate the degree of disturbance and the entry of organisms from soil, sewage and human contact. A simple diversity index, calculated from the genera identified in a sample, can supplement the usual counts of indicator organisms. Studies that combine counts with a diversity measure for household water sources are few, especially in small communities.

This study compares five types of household water source in terms of bacterial load, indicator organisms, turbidity and genus-level diversity. It asks whether these measures differ among sources, which genera characterise each source, and how bacterial load relates to turbidity and to diversity.

Literature Review

Drinking water guidelines define the standard for microbial safety. The World Health Organization requires that E. coli or thermotolerant coliforms should not be detectable in any 100 mL sample of water intended for drinking (WHO, 2017), and the Indian standard specifies the same absence of coliform organisms in drinking water (BIS, 2012). Edberg et al. (2000) reviewed indicator organisms and concluded that E. coli is the best biological indicator of faecal contamination for the protection of public health, because it is specific to the intestines of warm-blooded animals and can be detected readily.

Heterotrophic plate counts are used to describe the general bacterial content of water. Allen et al. (2004) reviewed their significance and concluded that they are not in themselves an indicator of health risk, but that they are useful for monitoring changes in water quality and the effectiveness of treatment. Hammes et al. (2010) showed that measurement of microbial ATP gives a more complete picture of the living biomass in water than plate counts, since most bacteria in water cannot be cultured on standard media. Proctor and Hammes (2015) argued that drinking water microbiology is moving from measurement of a few indicators to management of the whole microbial community.

Studies of community structure show that treatment and the distribution system shape the drinking water microbiome.

Pinto et al. (2012) found that the structure of bacterial communities was governed mainly by filtration processes, and that communities in treated water differed from those in source water. Such findings suggest that the origin and handling of water determine its biological character.

The risk of recontamination between source and home has been widely documented. Wright et al. (2004) reviewed studies from developing countries and found that water was often of better quality at the source than at the point of use, with contamination occurring during collection, transport and storage in the household. Bain et al. (2014) found a high frequency of faecal contamination in unprotected sources such as open wells, compared with piped supplies and protected sources.

The Shannon index, derived from information theory (Shannon, 1948), is widely used by ecologists to quantify diversity, and it combines the number of taxa and their relative abundance. Its application to household water sources at the genus level is rare.

The literature thus shows differences among sources and the importance of storage, but few studies report counts, indicators and a diversity index together in the same samples. This study fills that gap.

Research Methodology

Study area and sampling

The study was carried out in a mixed urban and peri-urban area. Five types of water source used for drinking were selected: piped municipal supply, borewell, hand pump, open dug well and water stored in household containers. Twenty-four samples were taken from each type, making 120 samples, at randomly selected sites over a period of three months. Samples were collected in sterile 500 mL bottles containing sodium thiosulphate for chlorinated supplies, taking care to avoid contamination, labelled, transported in a cool box and processed within six hours. Stored water samples were taken from containers in the household that had been filled at least 12 hours before.

Laboratory analysis

The total plate count was determined by the pour plate method on plate count agar at 37 °C for 48 hours and expressed as $\log_{10}$ colony-forming units per millilitre. Total coliforms were estimated by the multiple-tube fermentation method as the most probable number per 100 mL, and E. coli was confirmed on selective media and by biochemical tests, in accordance with Standard Methods (APHA, 2017). Turbidity was measured with a nephelometer in nephelometric turbidity units, and pH was recorded. Representative colonies of different morphology were isolated, purified and identified to genus level by Gram staining and standard biochemical tests. For each sample the genera identified were recorded as present or absent.

Diversity and statistical analysis

The Shannon diversity index, $H' = -\Sigma\, p_i \ln p_i$, was calculated for each sample using the relative frequency of each genus among the isolates identified (Shannon, 1948). Results are given as mean ± SD. Differences in continuous measures among sources were tested by one-way analysis of variance with Tukey–Kramer comparisons. The proportion of samples with E. coli was compared by chi-square, with Wilson 95% confidence intervals and Cramér's V. The relation between turbidity and bacterial load, and between diversity and bacterial load, was examined across the five sources by Pearson correlation. A p value below 0.05 was regarded as significant.

Table 1. Study hypotheses and tests

Hypothesis	Statement	Test
H1	Total plate count and coliforms differ among water sources	One-way ANOVA
H2	Shannon diversity differs among sources	One-way ANOVA
H3	Presence of E. coli differs among sources	Chi-square test
H4	Turbidity is related to bacterial load	Pearson correlation

Results

Bacterial load and coliforms

Total plate count differed significantly among sources ($F(4, 115) = 30.9$, $p < 0.001$, $\eta^2 = 0.52$). It was lowest in piped water (2.3 log CFU/mL) and highest in open wells (4.3), with stored water (3.8) and hand pumps (3.4) in between (Table 2, Figure 1). All sources differed from piped water (Tukey–Kramer $p < 0.05$), and open wells were higher than stored water, although that difference was not significant (Tukey–Kramer $p = 0.091$). Total coliforms followed the same order ($F(4, 115) = 22.1$, $p < 0.001$). H1 is supported.

Table 2. Microbial and physical measures by water source (mean ± SD, n = 24 per source)

Source	Plate count (log CFU/mL)	Coliforms (log MPN/100 mL +1)	Shannon H′	Turbidity (NTU)
Piped municipal	2.3 ± 0.6	0.6 ± 0.7	1.12 ± 0.22	0.9 ± 0.4
Borewell	2.9 ± 0.7	1.1 ± 0.8	1.35 ± 0.25	1.6 ± 0.7
Hand pump	3.4 ± 0.7	1.6 ± 0.9	1.52 ± 0.26	2.8 ± 1.1
Open dug well	4.3 ± 0.6	2.6 ± 0.8	1.88 ± 0.27	6.2 ± 2.0
Stored water	3.8 ± 0.8	2.1 ± 0.9	1.71 ± 0.28	3.5 ± 1.4
ANOVA F	30.9	22.1	32.2	64.8

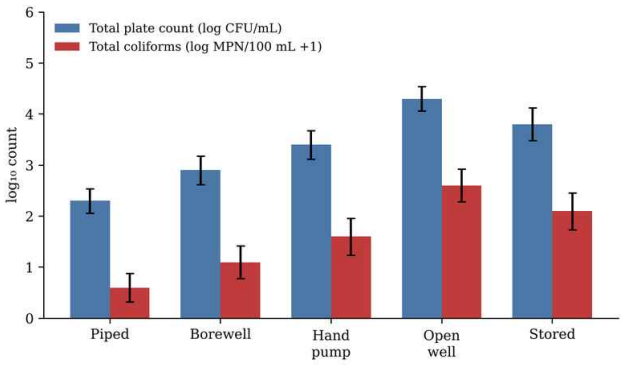


Figure 1. Total plate count and coliforms by water source (mean with 95% confidence intervals).

Escherichia coli

E. coli was detected in 39 of 120 samples (32.5%, 95% CI 24.8–41.3). Detection rose from 8.3% in piped water to 62.5% in open wells (Table 3, Figure 2; $\chi^2 = 21.0$, df = 4, $p < 0.001$; Cramér's V = 0.42). H3 is supported. Only the piped supply approached the guideline value of absence in 100 mL, and even there two samples were positive.

Table 3. Detection of Escherichia coli by water source (n = 24 per source)

Source	Positive, n	% (95% CI)
Piped municipal	2	8.3 (2.3–25.8)
Borewell	4	16.7 (6.7–35.9)
Hand pump	7	29.2 (14.9–49.2)
Open dug well	15	62.5 (42.7–78.8)
Stored water	11	45.8 (27.9–64.9)
All sources	39	32.5 (24.8–41.3)

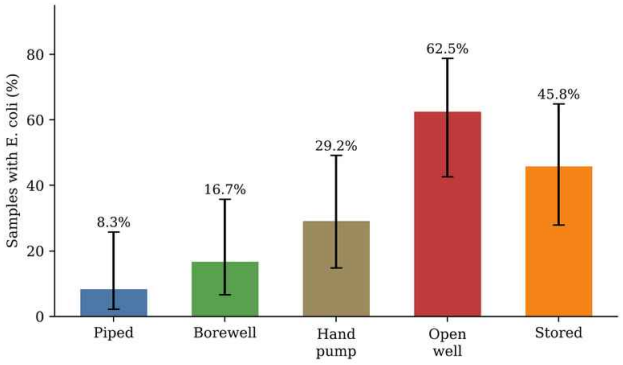


Figure 2. Percentage of samples positive for E. coli by water source (with 95% confidence intervals).

Microbial diversity and genera

The Shannon index differed significantly among sources ($F(4, 115) = 32.2$, $p < 0.001$, $\eta^2 = 0.53$). It was lowest in piped water (1.12) and highest in open wells (1.88), with stored water (1.71) second. Eight genera were detected in piped water and nine in each of the other sources. Pseudomonas and Bacillus were the most widely distributed genera, occurring in every source, whereas Escherichia, Klebsiella, Enterobacter and Aeromonas were found much more often in open wells and stored water (Table 4, Figure 3). Aeromonas was not found in piped water. H2 is supported.

Table 4. Frequency of bacterial genera by water source (% of 24 samples)

Genus	Piped	Borewell	Hand pump	Open well	Stored
Pseudomonas	38	50	58	79	71
Bacillus	33	46	62	75	54
Escherichia	8	17	29	62	46
Klebsiella	12	21	33	58	42
Enterobacter	12	25	38	54	50
Staphylococcus	4	8	17	33	38
Micrococcus	8	12	21	38	29
Aeromonas	0	12	21	46	25
Acinetobacter	8	12	21	25	33



Figure 3. Frequency of bacterial genera in each water source (percentage of samples positive).

Turbidity and bacterial load

Turbidity differed among sources ($F(4, 115) = 64.8$, $p < 0.001$), from 0.9 NTU in piped water to 6.2 NTU in open wells. Across the five sources, mean turbidity was strongly correlated with mean plate count ($r = 0.95$, $p = 0.012$), and mean Shannon index was strongly correlated with mean plate count ($r = 1.00$, $p < 0.001$). Each additional NTU of mean turbidity was associated with an increase of about 0.36 log CFU/mL. H4 is supported, although the correlations are based on five source means and should be seen as descriptive.

Discussion

Water source had a clear influence on the bacterial load and the diversity of household water. The gradient from piped water to protected groundwater to hand pumps, stored water and open wells corresponds to the degree of exposure of each source to surface contamination and handling. The high counts and frequent E. coli in open wells are consistent with reports that unprotected sources are the most frequently contaminated by faecal matter (Bain et al., 2014), since they are open to run-off, animals and human contact.

The result for stored water supports the conclusion that quality deteriorates between source and point of use (Wright et al., 2004). Stored water had higher counts, more coliforms and more E. coli than the piped supply from which it is likely to have been drawn, which indicates contamination during collection and storage through hands, utensils and open vessels. The finding indicates that source improvement alone is not enough and must be accompanied by safe storage and handling practice.

The Shannon index added information to the counts. Diversity rose with contamination, which suggests that the entry of organisms from soil, surface water and human sources increased the number of genera and the evenness of their distribution. Pseudomonas and Bacillus were widespread and are natural inhabitants of water and soil, which agrees with the view that a natural background community is present in all water (Allen et al., 2004). The concentration of enteric and opportunistic genera such as Escherichia, Klebsiella and Enterobacter in open wells and stored water is a more direct indicator of health risk. The finding that diversity and load rise together should not be taken to mean that greater diversity is beneficial; in drinking water it signals disturbance.

The association of turbidity with bacterial load is useful for practice. Particles shelter bacteria and reduce the effect of disinfection, and turbidity is simple to measure or to judge by eye, so it may serve as a quick screening indicator. The results also illustrate a limitation of plate counts, which capture only the culturable fraction (Hammes et al., 2010), and they point to the value of molecular methods in future work (Pinto et al., 2012; Proctor & Hammes, 2015).

Limitations

The study covered a single area and season, so seasonal changes in contamination, particularly in the monsoon, could not be examined. Identification was by morphology and biochemical tests to the genus level, which gives a partial view of diversity, and unculturable organisms were not captured. Twenty-four samples per source is a modest number, and the correlation analysis uses only five source means. Chemical contaminants and sanitary inspection scores, which affect microbial quality, were not recorded.

Conclusion

The source of household water has a strong influence on its microbial load and diversity. Piped water had the lowest counts and diversity, open wells the highest, and stored water was more contaminated than the piped supply. E. coli was detected in 32.5% of all samples and in 62.5% of open-well samples. Protection and treatment of sources, covered and clean storage, and household treatment such as boiling or filtration should be promoted, and routine monitoring should include turbidity as a simple screening measure. Further work should include seasonal sampling, molecular identification of communities and links with sanitary inspection and health outcomes.

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